wetland systems in the grassland biome of South Africa and is a Ramsar site. Nematodes were extracted from soil samples using the sugar-sieving-centrifugation-flotation method and fixed using standard techniques in preparation for light and scanning electron microscopy. Currently, nematodes are being identified and compared to the Juan Heyns reference material from the national Collection of Nematodes, Biosystematics Programme, Agricultural Research Council, , Pretoria. Results obtained to date include members from the genera *Dorylaimus*, *Mesodorylaimus, Prodorylaimus, Eudorylaimus* and *Allodorylaimus*. The aim of this study is to review all existing literature on the above-mentioned genera and to broaden the understanding of the taxonomy of this group of nematodesin South Africa.

VIRULENCE AND OXIDATIVE STRESS RESPONSE OF THE PINE WOOD NEMATODE *BURSAPHELENCHUS XYLOPHILUS*. **Vicente[1,2], C.S.L., Y. Ikuyo[1], R. Shinya[1,4], M. Mota[2,3], K. Hasegawa[1].** [1]Department of Environmental Biology, College of Bioscience & Biotechnology, Chubu University, 1200 Matsumoto, Kasugai, Aichi 487-8501, Japan; [2]ICAAM - Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Departamento de Biologia, Universidade de Évora, Núcleo da Mitra, Ap. 94, 7002-554 Évora, Portugal; [3]INIAV/Unidade Estratégica de Investigação e Serviços de Sistemas Agrários e Florestais e Sanidade Vegetal Av. da República, Quinta do Marquês 2784-159 Oeiras, Portugal; [4]HHMI and Division of Biology and Biological Engineering, California Institute of Technology, 1200 East California Blvd, Pasadena, California 91125, USA.

Bursaphelenchus xylophilus is the causal agent of pine wilt disease and the most devastating plant parasitic nematode attacking coniferous trees (mostly *Pinus* species) in the world. In the early stages of invasion, this nematode has to manage host defence mechanisms, such as strong oxidative stress. Only successful virulent nematodes are able to resist the basal immune plant counterattack, and further migrate and proliferate in numbers inside of the host tree. Our main objective was to study the oxidative stress tolerance of the virulent/avirulent *B. xylophilus* isolates and avirulent *Bursaphelenchus mucronatus*, and understand in which degree this feature is related with their virulence level. For this purpose, we used the most prominent reactive oxygen species H_2O_2 (hydrogen peroxide) as oxidative stress agent to evaluate the tolerance of the virulent/avirulent isolates of *B. xylophilus* and *B. mucronatus*, assessing catalase enzymatic activity, H_2O_2 neutralization and relative gene expression of different antioxidant enzymes. In addition, transgenic of *Caenorhabditis elegans* overexpressing *B. xylophilus* catalase were constructed and evaluated for survival under oxidative stress conditions. Here we show the correlation between *B. xylophilus* virulence and oxidative stress resistance; virulent *B. xylophilus* expressed more antioxidant enzymes and could have more tolerance against oxidative stress than avirulent *B. xylophilus* and *B. mucronatus*. Moreover, transgenic *C. elegans* overexpressing *B. xylophilus* catalase were able to resist better than wild type *C. elegans*. Our study suggests that oxidative stress tolerance of *B. xylophilus* is important to withstand against host plant counter-attack and can be considered a pathogenicity factor.

ECTOPIC EXPRESSION OF CELL CYCLE INHIBITOR GENES EFFECTIVELY INTERFERES WITH ROOT-KNOT NEMATODE FEEDING SITE DEVELOPMENT. **Vieira[1], P., N. Rodiuc[1], L. De Veylder[2], G. Engler[1,3], P. Abad[1], J. de Almeida Engler[1,4].** [1]Institut National de la Recherche Agronomique, UMR 1355 ISA/Centre National de la Recherche Scientifique, UMR 7254 ISA/Université de Nice-Sophia Antipolis, UMR ISA, 400 route des Chappes, Sophia-Antipolis, France; [2]Department of Plant Systems Biology, Flanders Institute for Biotechnology, Technologiepark 927, 9052 Gent, Belgium; [3]PVE-UCB/CAPES, Brasilia, Brazil; [4]PVE-UnB/CAPES, Brasilia, Brazil.

Root-knot nematodes (*Meloidogyne* spp.) modify plant root cells by inducing specialized feeding structures. Selected root vascular cells are changed to form complex feeding cells that supply nutrients for the nematodes to develop and reproduce. Giant-feeding cells are characterised by a dense cytoplasm filled with proliferating organelles The changes that occur during feeding cell morphogenesis are accompanied by a drastic rise in ploidy levels, metabolic activity and cell size. We have shown that activation of the cell cycle plays a key role in feeding site development but how precisely nematodes manipulate this process in their favour remains to be better comprehended. A systematic comparison of the temporal and spatial expression pattern of core cell cycle genes between galls and uninfected control roots of *Arabidopsis thaliana* resulted in the identification of a collection of genes up- or down regulated in nematode feeding sites. Their functional analyses resulted in the identification of a subset of genes strongly impairing gall development. The disruption of many *Arabidopsis* cell cycle regulators has been shown to affect both mitotic and endoreduplication cycles. Among them, negative regulators such as the ICK2/KRP2 gene are highly expressed during gall development and are candidates to control the cell cycle in NFC. ICK2/KRP2, a member of the cyclin-dependent kinase/kip-related proteins (ICK/KRP), regulates mitosis-to-endocycle transition in plant cells and is expressed in endoreduplicating cells. Herein we present data related with four KRP genes exerting different functions during feeding site development.

SYNERGISTIC INTERACTION BETWEEN PLANT-FEEDING NEMATODES AND THE FUNGUS *RHIZOCTONIA SOLANI* IN POTATO. **Viketoft[1], M. and E. Edin[2].** [1]Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Department of Forest Mycology and Plant Pathology, Uppsala, Sweden.